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Emmens, J. E.; Jones, Donald J. l.; Cao, T. H.; Chan, Daniel C. S.; Romaine, Simon P. R.; Quinn, Paulene A.

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# Proteomic diversity of high-density lipoprotein explains its association with clinical outcome in patients with heart failure

Emmens JE[1], Jones DJL[2], Cao TH[3,4], Chan DCS[3], Romaine SPR[3], Quinn PA[3], Anker SD[5,6], Cleland JG[7], Dickstein K[8,9], Filippatos G[10], Hillege HL[1], Lang CC[11], Ponikowski P[12], Samani NJ[3], Van Veldhuisen DJ[1], Zannad F[13], Zwinderman AH[14], Metra M[15], De Boer RA[1], Voors AA[1], Ng LL[3]

**Affiliations:**

[1] University of Groningen, University Medical Center Groningen, Department of Cardiology, Groningen, The Netherlands

[2] Department of Cancer Studies, University of Leicester, Leicester Royal Infirmary, Leicester, United Kingdom.

[3] Department of Cardiovascular Sciences, University of Leicester, Leicester, United Kingdom; NIHR Leicester Biomedical Research Centre, Glenfield Hospital, Leicester, LE3 9QP United Kingdom.

[4]Department of General Internal Medicine, University of Medicine and Pharmacy, Ho Chi Minh City, Vietnam

[5]Division of Cardiology and Metabolism – Heart Failure, Cachexia & Sarcopenia, Department of Cardiology (CVK); and Berlin-Brandenburg Center for Regenerative Therapies (BCRT); Deutsches Zentrum für Herz-Kreislauf-Forschung (DZHK) Berlin; Charité Universitätsmedizin Berlin, Germany.

[6]Department of Cardiology and Pneumology, University Medical Center Göttingen (UMG), Göttingen, Germany

[7]National Heart & Lung Institute, Royal Brompton and Harefield Hospitals, Imperial College, London, UK

[8]University of Bergen, Bergen, Norway

[9]Stavanger University Hospital, Stavanger, Norway

[10]National and Kapodistrian University of Athens, School of Medicine, Department of Cardiology, Heart Failure Unit, Athens University Hospital Attikon, Athens, Greece

[11]School of Medicine Centre for Cardiovascular and Lung Biology, Division of Medical Sciences, University of Dundee, Ninewells Hospital & Medical School, Dundee, UK

[12]Department of Heart Diseases, Wroclaw Medical University, Poland and Cardiology Department, Military Hospital, Wroclaw, Poland

[13]Inserm CIC 1433, Université de Lorrain, CHU de Nancy, Nancy, France

[14]Department of Epidemiology, Biostatistics and Bioinformatics, Academic Medical Centre, Amsterdam, the Netherlands

[15]Institute of Cardiology, Department of Medical and Surgical Specialties, Radiological Sciences and Public Health, University of Brescia, Italy

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**Corresponding author**

Prof. dr. L.L. Ng

Department of Cardiovascular Sciences

University of Leicester

Leicester

United Kingdom

NIHR Leicester Biomedical Research Centre

Glenfield Hospital

Leicester LE3 9QP

United Kingdom

Tel: 0116 250 2449

E-mail: lln1@le.ac.uk.

# Abstract

## Aims

Previously, low high-density lipoprotein (HDL) cholesterol was found to be one of the strongest predictors of mortality and/or heart failure (HF) hospitalisation in patients with HF. We therefore performed in-depth investigation of the multifunctional HDL proteome to reveal underlying pathophysiological mechanisms explaining the association between HDL and clinical outcome.

## Methods and results

We selected a cohort of 90 HF patients with 1:1 cardiovascular death/survivor ratio from BIOSTAT-CHF. A novel optimised protocol for selective enrichment of lipoproteins was used to prepare plasma. Enriched lipoprotein content of samples was analysed using high resolution nanoscale liquid chromatography-mass spectrometry-based proteomics, utilising a label free approach. Within the HDL proteome, 49 proteins significantly differed between deaths and survivors. An optimised model of 12 proteins predicted death with 76% accuracy (Nagelkerke $R^2 = 0.37$, P-value < 0.001). The strongest contributors to this model were filamin-A (related to crosslinking of actin filaments) (OR 0.31, 95% CI 0.15 – 0.61, P = 0.001) and pulmonary surfactant-associated protein B (related to alveolar capillary membrane function) (OR 2.50, 95% CI 1.57 – 3.98, P < 0.001). The model predicted mortality with an area under the curve of 0.82 (95% CI 0.77 – 0.87, P < 0.001). Internal cross validation resulted in 73.3 ± 7.2% accuracy.

## Conclusion

This study shows marked differences in composition of the HDL proteome between HF survivors and deaths. The strongest differences were seen in proteins reflecting crosslinking of actin filaments and alveolar capillary membrane function, posing potential pathophysiological mechanisms underlying the association between HDL and clinical outcome in HF.



**Key words: heart failure; high-density lipoprotein; proteome**

## Abbreviations

| | |
|---|---|
| **AHSG** | Alpha-2-HS-Glycoprotein |
| **APOA1** | Apolipoprotein A-I |
| **APOA2** | Apolipoprotein A-II |
| **APOC3** | Apolipoprotein C-III |
| **B2M** | Beta-2-Microglobulin |
| **BIOSTAT-CHF** | A systems BIOlogy Study to TAilored Treatment in Chronic Heart Failure |
| **BNP** | Brain Natriuretic Peptide |
| **eGFR** | Estimated Glomerular Filtration Rate |
| **EPHX1** | Epoxide Hydrolase 1 |
| **F10** | Coagulation Factor X |
| **FLNA** | Filamin-A |
| **HDL** | High-density Lipoprotein |
| **LVEF** | Left Ventricular Ejection Fraction |
| **MST1** | Macrophage-stimulating protein |
| **NT-proBNP** | N-Terminal Pro Brain Natriuretic Peptide |
| **NYHA** | New York Heart Association |
| **PON1** | Serum paraoxonase/arylesterase 1 |
| **SFTPB** | Pulmonary Surfactant-Associated Protein B |

# Introduction

Several studies showed that lower high-density lipoprotein (HDL) cholesterol was associated with a higher incidence of heart failure (HF),[1] worsening of HF,[2] and mortality and HF hospitalisation in patients with established HF.[2-5] We recently studied predictors of clinical outcome in two large European cohorts of patients with HF (BIOSTAT-CHF). Low HDL-cholesterol was found to be amongst the strongest independent predictors of death and/or HF hospitalisation.[6] The exact pathophysiological mechanisms underlying the association between HDL and HF are however unknown.

Technological developments and the use of mass spectrometry have strongly increased our understanding of the proteomic diversity of HDL. Besides the well-known function in reverse cholesterol transport, HDL carries many other constituents. Previous studies have identified over 90 proteins that are consistently co-expressed in variable amounts attached to HDL particles, consisting of apolipoproteins, lipid transfer proteins, enzymes, acute-phase response proteins, complement components, haemostasis proteins and several others. The functions of HDL are therefore multifold: it possesses anti-inflammatory, antioxidant, anti-infective, antithrombotic, and atheroprotective capacities and exerts effects on endothelial function.[7]

We hypothesised that further in-depth investigation of the multifunctional HDL proteome could reveal possible underlying pathophysiological mechanisms of HDL in HF that can help us understand its clinical value in HF. Therefore, this study aims to investigate differences in HDL proteome composition in HF that relate to a worse prognosis in HF.

# Materials & Methods

## Patient population

This study was conducted with patients selected from the A systems BIOlogy Study to TAilored Treatment in Chronic Heart Failure (BIOSTAT-CHF) cohort, which has been described in detail

before.[8] In brief, BIOSTAT-CHF was an investigator-driven multicentre clinical study consisting of 2516 patients which aimed to identify patients with a poor outcome despite currently recommended treatment using a systems biology approach that incorporates demographics, gender, biomarkers, genetics and proteomics. Patients were included after presentation with either new onset or worsening HF, which was confirmed by left ventricular ejection fraction (LVEF) ≤ 40% and/or brain natriuretic peptide (BNP) > 400 pg/mL or N-terminal pro brain natriuretic peptide (NT-proBNP) > 2000 pg/mL. All patients recruited in BIOSTAT-CHF gave written informed consent to participate in the study. BIOSTAT-CHF was conducted in concordance with the declaration of Helsinki, national ethics and legal requirements, as well as relevant EU legislation. The study was approved by national and local ethics committees.

For this study, 90 patients from BIOSTAT-CHF were selected for a discovery cohort and matched with a 1:1 death/survivor ratio of cardiovascular (CV) cause within a follow-up period of 12 months. Patients were furthermore matched for important prognostic criteria. The matching criteria and randomisation procedure are shown in supplementary material (Appendix 1).

**Sample preparation**

The detailed sample preparation protocol has been included in supplementary material (Appendix 2). Lipoproteins were isolated using calcium silicate matrix (commercial name Lipid Removal Agent (LRA), Sigma-Aldrich, St Louis, MO, USA), to separate them from other abundant proteins in plasma which will impair proteomic analysis. Prior to trypsin digestion, disulphide bonds were reduced using tris (2-carboxyethyl) phosphine (TCEP, Sigma-Aldrich), cysteines alkylated by iodoacetamide (IAA, Sigma-Aldrich), following denaturation using ammonium deoxycholate (ADC, 0.5%, deoxycholic acid treated with neat ammonium hydroxide, Sigma-Aldrich), thus allowing trypsin maximum access to the cleavage sites within the protein and preventing renaturation. Trypsin (Sigma-Aldrich) was added and the samples were incubated at 37 °C for 16h. Trypsin digestion was stopped by lowering the pH of the sample with a volume of fully concentrated formic acid (FA, final concentration 1%, Sigma-Aldrich). Salts and other undesired impurities were eliminated by solid phase extraction (SPE) on EMPORE C18 discs. A semi-pooled sample was created from 10 random samples of the discovery

cohort to serve as a Quality Control (QC) sample. The QC samples were treated equal to the other samples.

Samples were reconstituted in purified water containing FA (0.1%) and spiked with an internal standard, MassPREP™ yeast alcohol dehydrogenase (ADH, Waters Corporation, Manchester, UK), with a known amount of 50 fmol injected for each run; 1 µL of sample was injected. All samples were analysed in triplicate. A QC was run in triplicate after each batch of 10 samples with an injection volume of 1 µL for each single run. In between each patient or QC, washings were performed with three different cleaning mixtures that contained isopropyl alcohol, methanol, and FA respectively.

**Nanoscale Liquid Chromatography (LC)-coupled Mass Spectrometry**

Each sample was analysed on a Waters NanoAcquity system (Waters Corporation, Milford, MA, USA). The LC system was coupled to a Waters Synapt G2S HDMS (Waters Corporation, Milford, MA, USA). Data were acquired using MassLynx 4.1. Details on the settings and methodology that were implemented are described in supplementary material (Appendix 3).

**Data analysis**

Raw data were interrogated by Progenesis QI software (Nonlinear Dynamics, Gateshead, UK) for data analysis. A description of the used search criteria is included in supplementary material (Appendix 3). Progenesis QI executed label-free quantification of the identified proteins using the Hi-N3 method as first described by Silva et al.[9] Since the samples were internally spiked, this allowed for both Hi-N relative quantification and Hi-N absolute quantification. Analyses were focused on Hi-N relative quantification, with the Hi-N absolute quantification method serving as a verification back-up if needed.

**Statistical analysis**

Descriptive statistics were used to examine the relationship of the two groups with clinical variables. Prior to analyses, the distribution of all variables was checked. Data are presented as mean ± SD when normally distributed, as median (interquartile range) for skewed variables and as frequencies

(percentage) for categorical variables. A p-value of $< 0.05$ was considered statistically significant. Continuous normally distributed variables were tested with the student independent t-test or analysis of variance (ANOVA), whereas skewed variables were tested using the Kruskal-Wallis H test. Categorical variables were tested with Chi-Squared tests. To adjust for multiple testing, a false discovery rate of 1% was implemented for biomarker selection. Different search techniques (logistic regression and orthogonal projections to latent structures-discriminant analysis (OPLS-DA)) were used to establish an optimised model among significant proteins for death prediction. Logistic regression analysis of this optimised model was adjusted for age, sex, trigger event, trigger reason, LVEF, estimated glomerular filtration rate (eGFR), and CV death risk score, which are explained in further detail in Appendix 1. Statistical tests were performed with IBM SPSS Statistics version 23. SIMCA version 14 (MSK Umetrics, Sweden) was used to perform principal component analysis (PCA) and construct the S-plot. Internal cross validation was performed using RapidMiner software version 7.4 for candidate biomarkers. Gene Ontology analysis of proteins was executed using the Protein ANalysis THrough Evolutionary Relationships (PANTHER) Classification System version 11.1.[10]

# Results

### Patient characteristics

Patient characteristics of the two groups are displayed in Table 1. Mean age was 70.0 ± 9.3 in the patients who survived and 69.9 ± 8.8 years in the patients who died. In both groups, most patients were men (87%), most patients had a NYHA classification of III/IV (87% and 78% for survivors and deaths respectively), and HDL cholesterol levels were higher in the survivors group (1.1 (1.0 – 1.3) mmol/L, as opposed to 0.8 (0.7 – 1.1) mmol/L in deaths, P = 0.004). All other patient characteristics were not significantly different between the two groups. Mean study participation time was 787.0 ± 137.6 days for survivors and 151.7 ± 98.7 days for deaths.

### Principal component analysis

The separation of the HDL proteomes of survivors and deaths is indicated in Figure 1. Each point on the plot represents a patient's proteome profile (either deceased or survivor) based on the patient sample analysis in triplicate. The principal component analysis is also displayed in 2D in Supplementary Figure 1.

**HDL proteome biomarkers selection**

A total of 647 proteins with quantification were identified from both groups and compared. Out of all reported HDL proteins, as documented by the HDL Proteome Watch (initiated by the Davidson Lab, Cincinnati, OH; database version 14/8/2015), abundances of 49 HDL proteins were significantly different between deaths and survivors (Supplementary Table 1). Gene Ontology analysis of these proteins revealed involvement in multiple biological processes, such as cellular processes (e.g. cell communication), biological regulation (e.g. homeostatic process), metabolic processes (e.g. lipid metabolism, protein metabolic process), and response to stimulus (e.g. immune response, response to stress), as shown in Supplementary Figure 2.

An optimised model featuring 12 selected proteins was established, using different search techniques, to predict death. These 12 proteins included coagulation factor X (F10), epoxide hydrolase (EPHX1), filamin-A (FLNA), macrophage-stimulating protein (MST1; also called hepatocyte growth factor-like protein), pulmonary surfactant-associated protein B (SFTPB), and serum paraoxonase/arylesterase 1 (PON1) based on multiple regression analysis, and alpha-2-HS-glycoprotein (AHSG; also called fetuin-A), apolipoprotein A-I (APOA1), apolipoprotein A-II (APOA2), apolipoprotein C-III (APOC3), beta-2-microglobulin (B2M), and kallistatin (also called Serpin A4) based on OPLS-DA using a Variable Importance in Projection (VIP)-value >1 as cut-off value (data not shown). An overview with details on the proteins is provided in Table 2.

Multiple logistic regression analysis of this set of proteins resulted in an ability to predict death with 76% accuracy (Nagelkerke $R^2 = 0.365$, P-value for the model < 0.001). Table 3 shows the contribution of each protein to the prediction model, after correcting for the matching criteria. The proteins that significantly contributed to the prediction of death were SFTPB (OR 2.50, 95% CI 1.57 –

3.98, P < 0.001), FLNA (OR 0.31, 95% CI 0.15 – 0.61, P = 0.001), APOA1 (OR 0.43, 95% CI 0.25 – 0.73, P = 0.002), EPHX1 (OR 3.15, 95% CI 1.54 – 6.44, P = 0.002), PON1 (OR 0.55, 95% CI 0.35 – 0.88, P = 0.013), and F10 (OR 2.09, 95% CI 1.10 – 3.94, P = 0.024). Associations of FLNA and SFTPB with structural and functional parameters and biomarkers are presented in Supplementary Table 2.

To further confirm the value of the selected proteins, a S-plot was drafted (as presented in Figure 2) to provide a graphical representation of both the covariance and correlation structure between the selected proteins and the predictive score for death.

In linear regression analysis, these 12 proteins significantly predicted HDL cholesterol (P < 0.001), resulting in $R^2 = 0.579$.

When a receiver operating characteristic (ROC) curve was plotted for all selected proteins combined, this resulted in an AUC of 0.820 (95% CI 0.768 – 0.872, P < 0.001) and a maximum sensitivity and specificity of 0.763 and 0.756 respectively.
Internal cross validation resulted in 73.3 ± 7.2% accuracy.

## Discussion

In the present study, we demonstrate that the HDL proteome is different in heart failure patients who survived and those who died. The strongest differences were seen in proteins reflecting crosslinking of actin filaments and alveolar capillary membrane function. These marked differences in HDL-proteome composition between deaths and survivors might reveal the pathophysiological mechanisms underlying the association between HDL and clinical outcome in HF.

Previous studies investigating the HDL proteome in HF observed differences in proteome profiles between healthy subjects and HF patients and proteome profiles in HF patients associated with immune response.[11,12] Additionally, diminished anti-inflammatory,[13] antioxidant activity,[13-15] and cholesterol efflux capacity[16] of HDL have been implicated in HF and predicted adverse events. The present study is the first to investigate differences in HDL proteome profiles related to clinical

outcome in HF in a larger, well-characterised HF patient population with well-matched subgroups, utilising state-of-the-art nanoscale liquid chromatography-coupled mass spectrometry and powerful informatics to analyse the data.

Out of 49 HDL proteins that significantly differed between deaths and survivors, we selected 12 proteins to predict death based on multiple statistical approaches. These 12 proteins notably reflected, among others, processes related to atherogenesis, inflammation, and oxidative stress. Not much is known about their association with HF (outcome), but alpha-2-HS-glycoprotein (also called fetuin-A) levels were found to be lower in chronic HF patients,[17] lower levels of ApoA1 have been associated with worse prognosis in HF,[4-5] higher beta-2-microglobulin levels have been proposed a cardiovascular risk marker in HF,[18] and decreased PON1 activity and levels have been associated with HF and adverse outcomes in HF.[13,14,19] We will elaborate on FLNA, SFTPB, and ApoC3 in the next section.

The strongest contributors to the prediction model were filamin-A (FLNA) and pulmonary surfactant-associated protein B (SFTPB). We realise that the presence of these proteins in the HDL proteome is not direct proof for their presence in the heart, or for signalling in the heart, but nevertheless believe their presence may have functional consequences to the heart related to the associations we describe. First, FLNA is an actin-binding protein that plays a role in cell signalling functions, such as cell migration and organ development. Deficiency of FLNA is, among others, associated with severe cardiac malformation, suggesting an important function of FLNA in cardiac morphogenesis.[20] In a mouse model, endothelial deletion of FLNA resulted in a defective endothelial response and increased scar formation, leading to worse myocardial infarction-induced left ventricular dysfunction.[21] These unfavourable effects of FLNA deficiency appear to be reflected by the decreased abundances of FLNA in deaths in our study.

Second, higher levels of SFTPB in deaths could be explained by the presence of increased alveolar membrane damage in a worse HF disease state due to increased pulmonary pressure, resulting in oedema and subsequently in dyspnoea in HF. Levels of surfactant proteins in plasma, especially SFTPB, are suitable biomarkers to assess lung health and alveolar capillary membrane function,

because when damaged, surfactant proteins move into the blood.[22-24] It is thus logical for SFTPB to be higher in a worse HF disease state (reflecting increased congestion), which has moreover been shown in HF before.[25] Whether the HDL-bound portion of SFTPB compared to SFTPB levels in plasma is a better predictor of HF outcome is difficult to say since it is not entirely clear what portion of the total amount of SFTPB binds to HDL, but in a previous study investigating the HDL proteome in end-stage renal disease patients, HDL-bound SFTPB was associated with ESRD, while its plasma counterpart was comparable between ESRD patients and CKD stage 4 patients.[26] It is thus possible for the SFTPB HDL-bound portion to be different from its plasma counterpart, which could possibly also be the case in different HF disease states.

Although most findings in this study are in line with the expected observations, an unexpected finding was that ApoC3 levels were lower in deaths. Previous studies repeatedly showed that higher ApoC3 levels are consistent with higher cardiovascular event rates due to its atherogenic effects. This has however predominantly been investigated for non-HDL lipid particles (LDL and very low density lipoprotein (VLDL)) and total plasma; data on HDL ApoC3 are too limited and inconsistent to confirm that the same is true for these particles.[27] However, as explained further on, a satisfactory explanation for this finding remains uncertain due to recovery of all lipoproteins by the used methodology.

**Strengths and limitations of the study**

This is the first study investigating HDL proteome composition in relation to clinical outcome in patients with HF. The lipoprotein isolation method that was used in this study proved to be highly suitable for addressing the aim of this study; we were able to detect 88.4% out of the total number of confident HDL proteins.

Furthermore, use of UPLC-HDMS$^E$ as a means to analyse proteins ensured high selectivity, specificity and confidence. The methods of this study proved to be time-efficient, high-throughput, reproducible, capable of working with complex samples and inexpensive (both the sample preparation procedure and the label-free quantification approach). Reliability of the MS runs was ensured by running quality controls and Hela cell extract and, on top of that, use of powerful informatics to

analyse the raw data. Finally, the well-matched groups ensured suitable circumstances for discovery purposes.

The fact that the survivors and the deaths groups were so well matched could however also pose a limitation: after correction for important influential factors such as age and severity of HF in a non-matched patient cohort, the HDL proteome may lose some of its predictive value. The matching used in this study cohort also limited analysis of the additive value of the HDL proteome on top of the recently constructed BIOSTAT risk score,[6] since the groups were already matched on some of the variables present.

Also, the results of this study only apply to patients of Caucasian ethnicity and HF patients with a reduced ejection fraction.

Furthermore, the lipid affinity matrix used in this study does not have specific affinity for HDL alone and other lipid subclasses could have potentially influenced the measured apolipoprotein amounts to some extent.

Finally, only 49 patients had available HDL cholesterol measurements. However, we do not know whether the HDL protein to cholesterol ratio is similar for every patient, which is why there is no indication to say that this has certainly influenced our results. Furthermore, we have loaded equal total peptide amounts on the LC-MS/MS for each sample. As a surrogate for HDL cholesterol, ApoA1 is often used. We see in our analysis that ApoA1 is lower in deaths in univariate and multivariate analysis, which is in line with the association between lower HDL cholesterol and adverse outcome in HF in the BIOSTAT-CHF study.

In order to address some limitations of this study, the following studies could be carried out: a) a validation study to confirm the findings of this study in another study population; b) a study investigating the relationship between HDL functionality in relation with HDL proteome content and in relation to prognosis in HF; c) a validation of the total plasma content of FLNA and SFTPB where bound and free fractions can be calculated and independently related to outcomes, and d) addition of HF hospitalisation as an endpoint.

## Conclusions and implications

This study shows that abundances of proteins with multiple important functions that reflect, among others, atherogenesis, inflammation, and oxidative stress, are altered in the HDL proteome of patients with a worse HF disease state. The strongest differences were seen in proteins reflecting crosslinking of actin filaments and alveolar capillary membrane function. Therefore, HDL could be a proxy for these processes implicated in HF pathophysiology which might explain the association between low HDL and increased risk of mortality and/or hospitalisation in patients with HF.

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## Conflicts of interest

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# Figure Legends

**Figure 1. Principal component analysis of the HDL proteomes of survivors and deaths**

SIMCA14 was used to generate a 3D plot based on the OPLS-DA scores. Each data point represents a sample in the data. Each green point on the plot represents a survivor's proteome profile and each blue point represents a deceased patient's proteome profile, showing the separation of proteome profiles between survivors and deaths.

**Figure 2. S-plot of HDL proteins**

SIMCA14 was used to generate this figure based on OPLS-DA scores for putative biomarker identification. In this figure, the p1-axis (x-axis) describes the magnitude of each variable in the data and the p(corr)1-axis (y-axis) represents the reliability of each variable in the data. The selected proteins are indicated in red while the remaining significantly different proteins between deaths and survivors are indicated in green. Abbreviations: AHSG, alpha-2-HS-glycoprotein; APOA1, apolipoprotein A-I; APOA2, apolipoprotein A-II; APOC3, apolipoprotein C-III; B2M, beta-2-microglobulin; EPHX1, epoxide hydrolase 1; F10, coagulation factor X; FLNA, filamin-A; MST1, macrophage-stimulating protein; PON1, serum paraoxonase/arylesterase 1; SERPINA4, kallistatin; SFTPB, pulmonary surfactant-associated protein B.

**Figure 3. ROC curve for prediction of death**

Blue curve represents all 12 selected proteins combined.

# Appendix 1. Patient matching and randomisation procedure

## Patient matching

Patients were matched for important prognostic criteria including age (within 5 years difference), sex (exact matching), trigger event (exact matching), trigger reason (exact matching), LVEF (within 10% difference), eGFR, as calculated by the MDRD formula (within 50 mL $min^{-1}/1.73\ m^2$ difference, notional), and a risk score for CV death (regression-based score which included age, sex, eGFR, HF aetiology (ischaemic vs non-ischaemic), body mass index (BMI), HF hospitalisation within the year preceding recruitment, and New York Heart Association (NYHA) class; it was generated following multiple imputation using chained equations, creating five imputed datasets, after which the analysis was repeated for each dataset and residuals from each of the five models averaged to generate a final risk score for each individual that had to be within 0.25 difference between groups).

Additional criteria that were implemented for patient selection included ischemic aetiology and Caucasian ethnic origin, to reduce heterogeneity between study groups. In order to ensure data availability for patient matching and/or subsequent analyses, all patients entering selection were required to have a clear description of the reason for recruitment, and availability of data for NYHA class, eGFR, BMI, BNP and LVEF. To improve data quality, patients were also required to be concordant with all study criteria, have a recent echocardiogram and an exact date of death recorded (where applicable).

## Randomisation procedure

After the selection of patients all samples were allocated a randomised "Discovery ID", which was achieved as follows:

First, a list of BIOSTAT-CHF 'Patient IDs' was generated for discovery samples that were 'cases' and sorted into numerical order. The order of this list was then randomised using the 'List Randomizer' available at: https://www.random.org and these samples were paired with their matched 'controls' to generate case/control units (CCUs). A list of integers of either 1 or 2 was then generated using the 'Random Integer Generator'. Consequently, the samples from the CCUs were placed in a single list in the randomised order, with the integers 1 and 2 determining whether the case (1) or

control (2) entered the list first. Finally, samples were allocated a “Discovery ID” in ascending order from the randomised list order. This method of randomisation ensured that when processed in “Discovery ID” order, every 2 samples contains a case with its matched control, but this did not follow a predictable pattern of case, control, case, control, etc.

## Appendix 2. Protocol for MS sample preparation

1. Bind 50 µL plasma to 100 µL of 3 times pre-washed LRA (100 mg/mL stock solution) in 50 mM ammonium bicarbonate for 1 hour.

2. Wash tube in ammonium bicarbonate 5 times.

3. Add 10 mM TCEP at 60°C for 5 minutes.

4. Add 15 mM IAA at room temperature for 30 minutes in the dark.

5. Add 0.5% ADC for 30 minutes at 60°C.

6. Add trypsin 1:50 (trypsin to total expected amount of protein, calculated in weight of protein per tube) and incubate overnight at 37°C on a shaker plate. Approximate 4 mg of protein is assumed to be present in each sample.

7. Stop the trypsin by adding fully concentrated formic acid (FA, final concentration 1%).

8. Spin the sample hard and take off the peptides in the supernatant.

9. Empore samples to get rid of the salts. First, clean the columns with 1 mL of methanol and subsequently by 4 times 1 mL of 0.1% FA in water. Then load the samples onto the column to extract the peptides and subsequently wash with another 5 times 1 mL of 0.1% FA. Elute the extracted peptides with 0.9 mL of 60% acetonitrile (ACN) + 0.1% FA and 0.9 mL of 80% ACN + 0.1% FA and collect in 5 mL tubes.

10. Split the sample into 2 tubes, put one in freezer at -80ºC to serve as a back-up.

11. Speed vacuum the other tube for 2 hours.

12. Freeze dry overnight.

13. Suspend in 20 µL of purified water.

14. Perform a peptide assay.

15. Take 10 µL of the sample and mix with 10 µL 100 fmol ADH (made up in 0.2% FA in purified water), thus resulting in 50 fmol ADH in 0.1% FA (in purified water) per sample.

# Appendix 3. Nanoscale liquid chromatography-coupled mass spectrometry

**Nanoscale liquid chromatography(LC)**

The peptides were initially loaded onto a Symmetry C18 180 µm x 20 mm 5 µm trap column to desalt and chromatographically focus the peptides prior to elution onto a HSS T3 C18 75 µm x 150 mm, 1.7 µm analytical column. Solvent A: HPLC grade water with 0.1% formic acid and Solvent B: Acetonitrile with 0.1% formic acid was used. The flow rate was set at 0.3 µL/min. The gradient began following a 3 min (5 µL/min) trapping stage on the trap column. At time zero, A was 99% while B was 1%. B increased linearly to 40% at 90 min and to 85% at 92 min. The gradient was held at 85% B at 93 min and returned to starting conditions at 95 mins to equilibrate.

**Mass spectrometry**

The instrument was run in positive ion nanoelectrospray ionisation mode. Capillary voltage was set at 3.4 kV and cone voltage at 30 V. Picotip emitters (10 µm internal diameter, Presearch, Basingstoke, UK) were used for the nanostage to direct flow from the analytical column through to the source. A helium gas flow of 180mL/min and ion mobility (IM) separator gas flow ($N_2$) of 90 mL/min with a pressure of 2.5 mbar was used. An IM wave velocity of 600 m/s and wave height of 40 V was used throughout each run. During LC-IM-DIA-MS low collision-induced dissociation (CID) energy, 2 V was applied across the transfer ion guide. During high CID energy, a ramp of 27-50 V was applied. Argon was used as CID gas. Lockspray of [Glu1]-Fibrinopeptide (GFP) m/z at 785.84265 was used to maintain mass accuracy throughout the chromatographic run.

**Search criteria for data analysis**

Search criteria assumed trypsin digestion and included carbamidomethyl C as a fixed modification and deamidation N, oxidation M, and phorphoryl STY as variable modifications. The allowed number of missed cleavages was set to 2, minimal fragment ion matches per peptide and minimal fragment ion matches per protein was set to 2 and 5 respectively, minimal peptide matches per protein was set to 2, maximum hits to return was set to 20, and maximum protein mass was set to 1000 kDa. A false discovery rate of 1% was implemented. Processing parameters included 785.84265 Da as the set lock

mass, lock mass window 0.25, low energy threshold 150 counts, elevated energy threshold 25 counts, and intensity threshold 750 counts. These processing parameters were determined by optimisation using Protein Lynx Global Server Threshold Inspector (Waters Corporation, Manchester, UK).

**Table 1. Baseline characteristics of the BIOSTAT-CHF discovery cohort**

| **Characteristics** | **Survivors (*n* = 45)** | **Deaths (*n* = 45)** | **P-value** |
|---|---|---|---|
| Age (years) | 70.0 ± 9.3 | 69.9 ± 8.8 | 0.963 |
| Male sex, *n* (%) | 39 (87) | 39 (87) | 1.000 |
| BMI ($kg/m^2$) | 28.2 ± 4.8 | 27.5 ± 6.2 | 0.524 |
| NYHA class III/IV, *n* (%) | 39 (87) | 35 (78) | 0.524 |
| LVEF (%) | 28.0 ± 5.7 | 26.3 ± 7.2 | 0.221 |
| Systolic blood pressure (mmHg) | 124.5 ± 23.6 | 118.5 ± 21.3 | 0.210 |
| Diastolic blood pressure (mmHg) | 73.8 ± 13.7 | 72.3 ± 11.3 | 0.576 |
| Heart rate (bpm) | 76 ± 20 | 79 ± 15 | 0.440 |
| BNP (pg/mL) | 409.3 (162.0 – 573.2) | 488.4 (230.5 – 766.5) | 0.255 |
| eGFR ($ml/min^{-1}$) | 56.3 ± 17.2 | 53.2 ± 21.1 | 0.455 |
| Serum creatinine (µmol/L) | 114.0 (98.0 – 133.9) | 124.0 (99.7 – 163.5) | 0.296 |
| Total cholesterol (mmol/L)* | 3.7 (3.3 – 4.5) | 3.2 (2.8 – 4.2) | 0.070 |
| HDL cholesterol (mmol/L)** | 1.1 (1.0 – 1.3) | 0.8 (0.7 – 1.1) | **0.004** |
| LDL cholesterol (mmol/L)*** | 2.2 (1.7 – 3.2) | 1.8 (1.5 – 2.8) | 0.092 |
| Diabetes, *n* (%) | 20 (44) | 18 (40) | 0.670 |
| Hypertension, *n* (%) | 34 (76) | 27 (60) | 0.114 |
| Reason for visit, *n* (%)<br>- New onset of HF<br>- Worsening HF | <br>3 (7)<br>42 (93) | <br>3 (7)<br>42 (93) | <br>1.000 |

BMI, body mass index; BNP, brain natriuretic peptide; eGFR, estimated glomerular filtration rate; HDL, high density lipoprotein; HF, heart failure; LDL, low density lipoprotein; LVEF, left ventricular ejection fraction; NYHA, New York Heart Association.

* Data only available for 54 patients (28 survivors; 26 deaths)

** Data only available for 49 patients (26 survivors; 23 deaths)

*** Data only available for 48 patients (25 survivors; 23 deaths)

**Table 2. Proteins associated with clinical outcome in HF as selected by multiple approaches**

| Protein | Function | Higher or lower in deaths | Fold change | P-value |
|---|---|---|---|---|
| Alpha-2-HS-glycoprotein | Negative acute phase reactant | Lower | 1.18 | 0.014 |
| Apolipoprotein A-I | Anti-atherogenic, antioxidant, anti-inflammatory | Lower | 1.16 | <0.001 |
| Apolipoprotein A-II | Anti-atherogenic, antioxidant | Lower | 1.28 | 0.022 |
| Apolipoprotein C-III | Pro-atherogenic | Lower | 1.58 | 0.008 |
| Beta-2-microglobulin | Indicator of immune activation | Higher | 1.17 | 0.045 |
| Coagulation factor X | Coagulation | Higher | 1.22 | 0.021 |
| Epoxide hydrolase 1 | Detoxification | Higher | 1.17 | 0.008 |
| Filamin-A | Crosslinks actin filaments | Lower | 1.19 | 0.011 |
| Kallistatin | Antioxidant, anti-inflammatory, anti-fibrotic | Lower | 1.27 | <0.001 |
| Macrophage-stimulating protein | Stress response, pro-apoptotic | Lower | 1.26 | 0.034 |

| | | | | |
|---|---|---|---|---|
| Pulmonary surfactant-associated protein B | Assembly of pulmonary surfactant | Higher | 1.39 | 0.006 |
| Serum paraoxonase/arylesterase 1 | Anti-atherogenic, antioxidant, anti-inflammatory | Lower | 1.20 | 0.006 |

**Table 3. Multiple logistic regression model for prediction of death**

| Protein | B | Wald | P-value | Odds ratio (95% CI) |
|---|---|---|---|---|
| Alpha-2-HS-glycoprotein | -0.161 | 0.143 | 0.706 | 0.85 (0.37 – 1.96) |
| Apolipoprotein A-I | -0.846 | 9.926 | 0.002 | 0.43 (0.25 – 0.73) |
| Apolipoprotein A-II | 0.014 | 0.002 | 0.962 | 1.01 (0.58 – 1.77) |
| Apolipoprotein C-III | -0.159 | 0.513 | 0.474 | 0.85 (0.55 – 1.32) |
| Beta-2-microglobulin | 0.370 | 1.751 | 0.186 | 1.45 (0.84 – 2.50) |
| Coagulation factor X | 0.735 | 5.123 | 0.024 | 2.09 (1.10 – 3.94) |
| Epoxide hydrolase 1 | 1.147 | 9.875 | 0.002 | 3.15 (1.54 – 6.44) |
| Filamin-A | -1.186 | 11.350 | 0.001 | 0.31 (0.15 – 0.61) |
| Kallistatin | -0.285 | 1.225 | 0.268 | 0.75 (0.45 – 1.25) |
| Macrophage-stimulating protein | -0.198 | 0.626 | 0.429 | 0.82 (0.50 – 1.34) |
| Pulmonary surfactant-associated protein B | 0.916 | 14.917 | <0.001 | 2.50 (1.57 – 3.98) |
| Serum paraoxonase/arylesterase 1 | -0.592 | 6.216 | 0.013 | 0.55 (0.35 – 0.88) |

**Figure 1. Principal component analysis of the HDL proteomes of survivors and deaths**

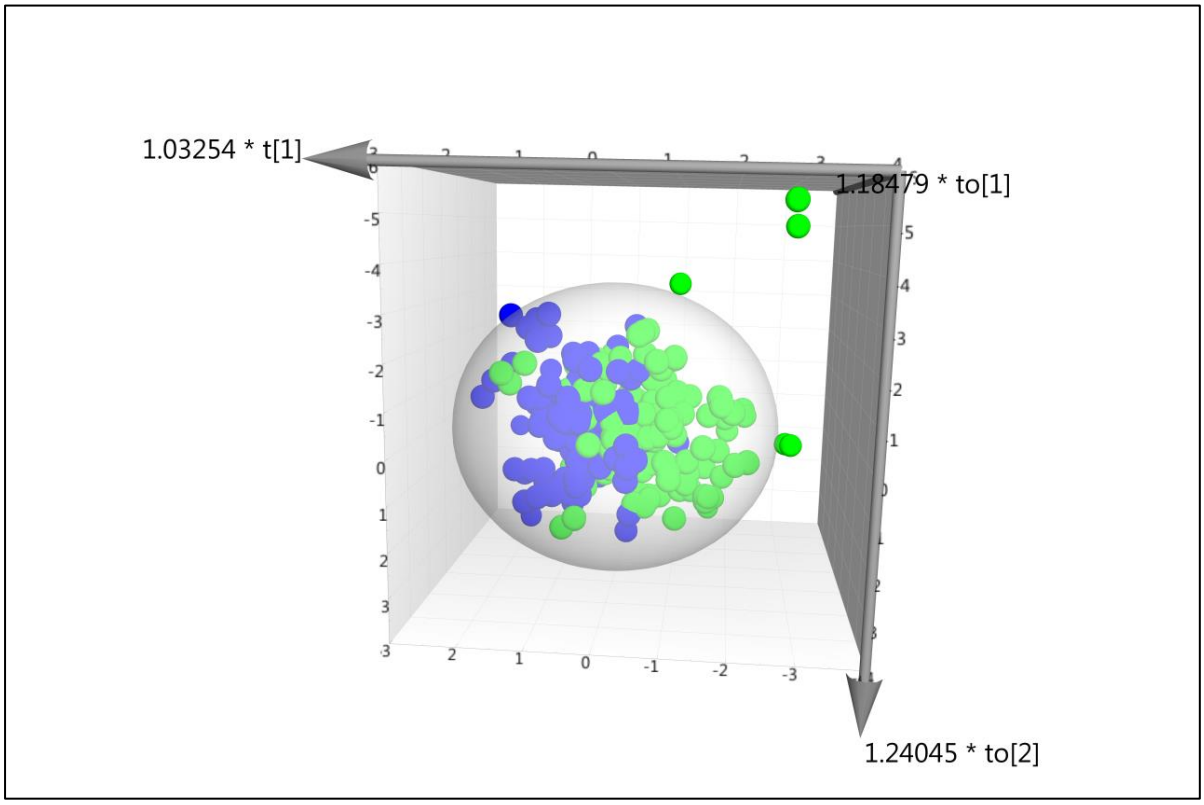


**Figure 2. S-plot of HDL proteins**

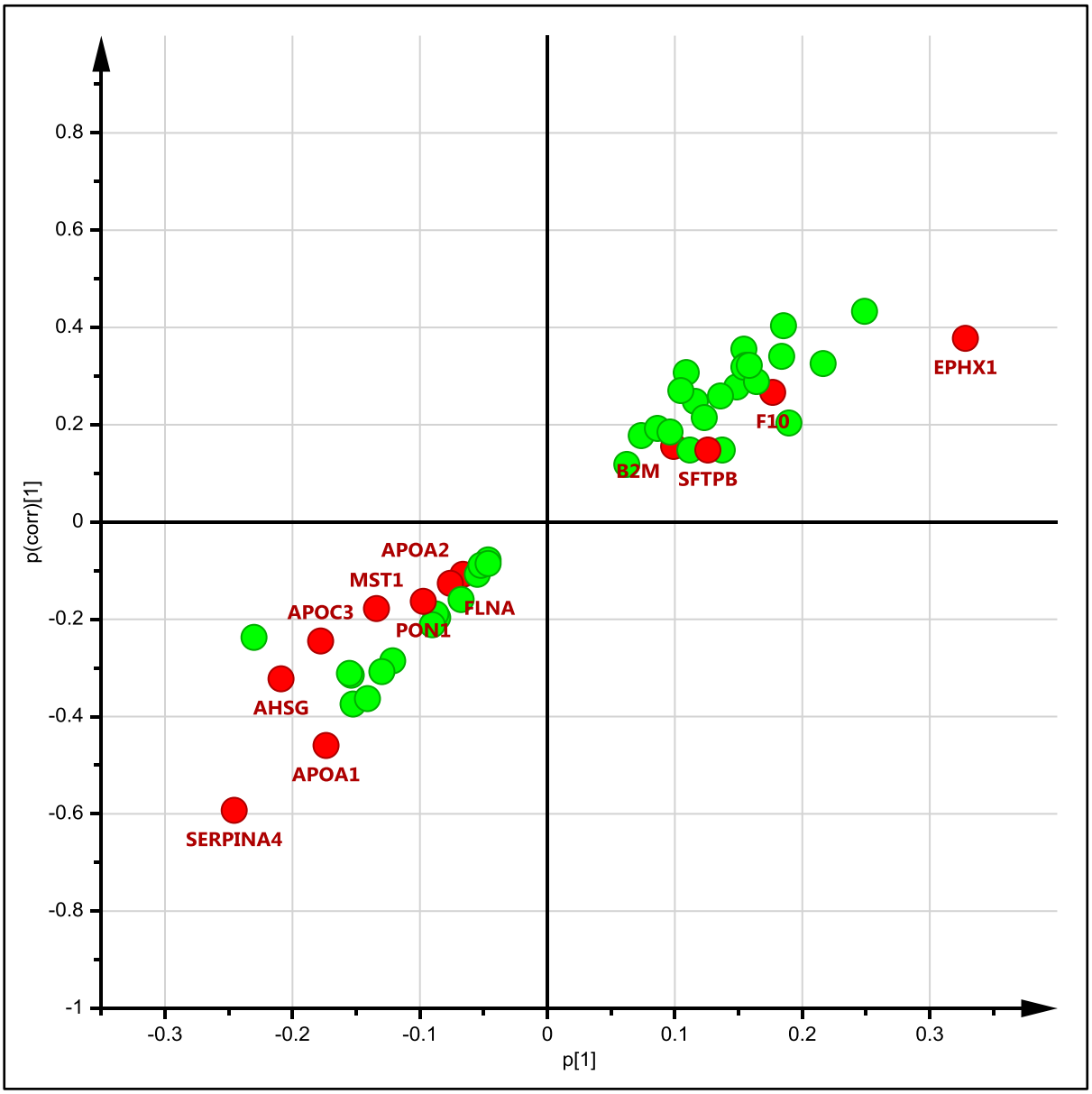
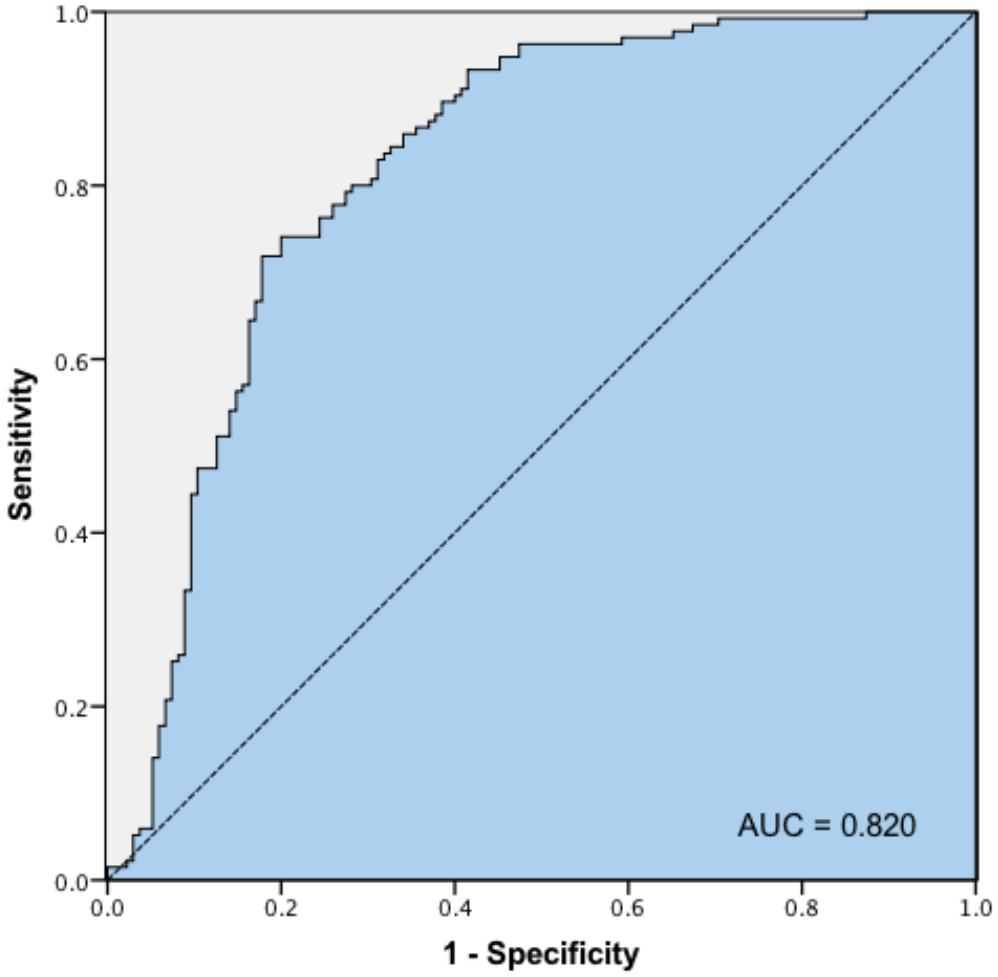


**Figure 3. ROC curve for prediction of death**



**Supplementary material**

**Supplementary Table 1. All significantly different HDL proteins between deaths and survivors**

| Accession number | Protein | Highest condition | Fold change | P-value |
|---|---|---|---|---|
| Q9HDC9 | Adipocyte plasma membrane-associated protein | Deaths | 1.12 | 0.027 |
| P19652 | Alpha-1-acid glycoprotein 2 | Survivors | 1.12 | 0.041 |
| P01011 | Alpha-1-antichymotrypsin | Deaths | 1.13 | 0.001 |
| P01009 | Alpha-1-antitrypsin | Deaths | 1.21 | <0.001 |
| P04217 | Alpha-1B-glycoprotein | Deaths | 1.15 | 0.004 |
| P02765 | Alpha-2-HS-glycoprotein | Survivors | 1.18 | 0.014 |
| P01023 | Alpha-2-macroglobulin | Deaths | 1.09 | 0.007 |
| P02647 | Apolipoprotein A-I | Survivors | 1.16 | <0.001 |
| P02652 | Apolipoprotein A-II | Survivors | 1.28 | 0.022 |
| P04114 | Apolipoprotein B-100 | Deaths | 1.07 | 0.020 |
| P02656 | Apolipoprotein C-III | Survivors | 1.58 | 0.009 |
| P61769 | Beta-2-microglobulin | Deaths | 1.17 | 0.045 |
| P00450 | Ceruloplasmin | Deaths | 1.22 | <0.001 |
| P12259 | Coagulation factor V | Deaths | 1.15 | 0.019 |
| P00742 | Coagulation factor X | Deaths | 1.22 | 0.022 |
| P12111 | Collagen alpha-3(VI) chain | Deaths | 1.11 | 0.015 |
| P07357 | Complement component C8 alpha chain | Survivors | 1.29 | <0.001 |
| Q02985 | Complement factor H-related protein 3 | Survivors | 1.15 | 0.049 |
| P07099 | Epoxide hydrolase 1 | Deaths | 1.17 | 0.008 |
| P21333 | Filamin-A | Survivors | 1.19 | 0.011 |

| | | | | |
|---|---|---|---|---|
| P06396 | Gelsolin | Survivors | 1.12 | 0.016 |
| Q8WU03 | Glycine N-acyltransferase-like protein 2 | Survivors | 1.53 | 0.021 |
| P26927 | Hepatocyte growth factor-like protein | Survivors | 1.26 | 0.034 |
| P04196 | Histidine-rich glycoprotein | Survivors | 1.18 | 0.023 |
| Q14520 | Hyaluronan-binding protein 2 | Survivors | 1.08 | 0.027 |
| P01876 | Ig alpha-1 chain C region | Deaths | 1.24 | <0.001 |
| P01877 | Ig alpha-2 chain C region | Deaths | 1.21 | <0.001 |
| P01880 | Ig delta chain C region | Survivors | 1.17 | 0.002 |
| P01860 | Ig gamma-3 chain C region | Deaths | 1.16 | 0.046 |
| P01593 | Ig kappa chain V-I region AG | Survivors | 2.11 | 0.014 |
| P01620 | Ig kappa chain V-III region SIE | Survivors | 1.06 | 0.040 |
| P04433 | Ig kappa chain V-III region VG (Fragment) | Deaths | 1.20 | 0.345917917 |
| P80748 | Ig lambda chain V-III region LOI | Deaths | 1.44 | <0.001 |
| B9A064 | Immunoglobulin lambda-like polypeptide 5 | Deaths | 1.16 | 0.032 |
| P29622 | Kallistatin | Survivors | 1.27 | <0.001 |
| P51884 | Lumican | Survivors | 1.14 | 0.037 |
| P61626 | Lysozyme C | Survivors | 1.19 | 0.002 |
| Q96PD5 | N-acetylmuramoyl-L-alanine amidase | Deaths | 1.08 | 0.029 |
| P36955 | Pigment epithelium-derived factor | Deaths | 1.19 | 0.015 |
| P03952 | Plasma kallikrein | Survivors | 1.13 | 0.035 |
| P00747 | Plasminogen | Survivors | 1.11 | 0.074 |
| Q9UK55 | Protein Z-dependent protease inhibitor | Deaths | 1.20 | 0.001 |
| P07988 | Pulmonary surfactant-associated protein B | Deaths | 1.39 | 0.006 |

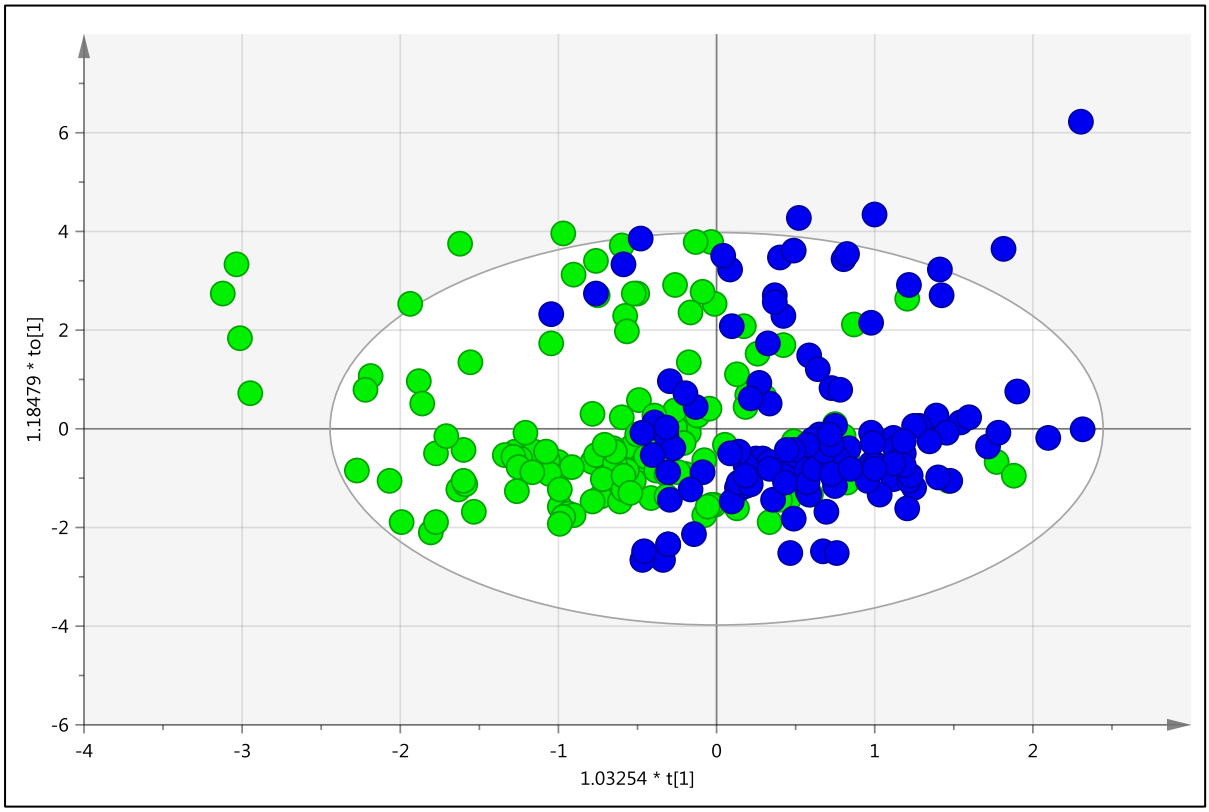
| | | | | |
|---|---|---|---|---|
| P62820 | Ras-related protein Rab-1A | Deaths | 1.14 | 0.019 |
| P02787 | Serotransferrin | Deaths | 1.16 | 0.042 |
| P02768 | Serum albumin | Survivors | 1.17 | 0.029 |
| P0DJI8 | Serum amyloid A-1 protein | Survivors | 1.05 | 0.033 |
| P27169 | Serum paraoxonase/arylesterase 1 | Survivors | 1.20 | 0.006 |
| P04004 | Vitronectin | Survivors | 1.11 | 0.024 |

**Supplementary Table 2. Correlations of FLNA and SFTPB with structural and functional parameters and biomarkers of inflammation, myocardial necrosis and wall strain**

| | Spearman's rho | | Spearman's rho | |
|---|---|---|---|---|
| **Variable** | **FLNA** | **P-value** | **SFTPB** | **P-value** |
| LVEDD* (mm) | -0.132 | 0.043 | -0.067 | 0.309 |
| LVESD** (mm) | -0.056 | 0.463 | -0.148 | 0.052 |
| LVEF (%) | -0.030 | 0.626 | -0.041 | 0.498 |
| E/A ratio† | -0.053 | 0.647 | -0.169 | 0.139 |
| CRP (ng/mL) | -0.303 | <0.001 | -0.021 | 0.734 |
| Troponin I (pg/mL) | 0.006 | 0.917 | 0.024 | 0.699 |
| ST-2 (ng/mL) | -0.035 | 0.570 | 0.238 | <0.001 |
| NT-proBNP‡ (pg/mL) | 0.170 | 0.079 | 0.052 | 0.593 |

*Data limited to 78 patients
**Data limited to 58 patients
†Data limited to 26 patients
‡Data limited to 36 patients

**Supplementary Figure 1. Principal component analysis of HDL proteins**




(Green: survivors, blue: deaths)

**Supplementary Figure 2. Biological processes associated with altered HDL proteome{** EMBED Prism7.Document **}**